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2/14

7 OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/935,726

DATE: 02/07/2002

TIME: 13:34:45

Input Set : A:\PF112P3D1C1subSL.txt

Output Set : N:\CRF3\02072002\I935726.raw

p.s

ENTERED

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3 <110> APPLICANT: Hu, Jin-Shan
4      Craig, Rosen
5      Cao, Liang
7 <120> TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
9 <130> FILE REFERENCE: PF112P3D1C1
11 <140> CURRENT APPLICATION NUMBER: 09/935,726
12 <141> CURRENT FILING DATE: 2001-08-24
14 <150> PRIOR APPLICATION NUMBER: 09/438,538
15 <151> PRIOR FILING DATE: 1999-11-12
17 <160> NUMBER OF SEQ ID NOS: 35
19 <170> SOFTWARE: PatentIn version 3.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1674
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
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27 <221> NAME/KEY: sig_peptide
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35 <221> NAME/KEY: mat_peptide
36 <222> LOCATION: (81)..()
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40      Met His Ser Leu Gly Phe Phe Ser Val Ala Cys Ser Leu
41      -20                      -15
43 ctc gcc gct gcg ctg ctc ccg ggt cct cgc gag gcg ccc gcc gcc gcc      98
44 Leu Ala Ala Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala
45 -10                      -5          -1 1          5
47 gcc gcc ttc gag tcc gga ctc gac ctc tcg gac gcg gag ccc gac gcg      146
48 Ala Ala Phe Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala
49      10                      15          20
51 gcc gag gcc acg gct tat gca agc aaa gat ctg gag gag cag tta cgg      194
52 Gly Glu Ala Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg
53      25                      30          35
55 tct gtg tcc agt gta gat gaa ctc atg act gta ctc tac cca gaa tat      242
56 Ser Val Ser Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr
57      40                      45          50
59 tgg aaa atg tac aag tgt cag cta agg aaa gga gcc tgg caa cat aac      290
60 Trp Lys Met Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn
61 55                      60          65          70

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63 aga gaa cag gcc aac ctc aac tca agg aca gaa gag act ata aaa ttt      338
64 Arg Glu Gln Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe
65              75              80              85
67 gct gca gca cat tat aat aca gag atc ttg aaa agt att gat aat gag      386
68 Ala Ala Ala His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu
69              90              95              100
71 tgg aga aag act caa tgc atg cca cgg gag gtg tgt ata gat gtg ggg      434
72 Trp Arg Lys Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly
73              105              110              115
75 aag gag ttt gga gtc gcg aca aac acc ttc ttt aaa cct cca tgt gtg      482
76 Lys Glu Phe Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val
77              120              125              130
79 tcc gtc tac aga tgt ggg ggt tgc tgc aat agt gag ggg ctg cag tgc      530
80 Ser Val Tyr Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys
81 135              140              145              150
83 atg aac acc agc acg agc tac ctc agc aag acg tta ttt gaa att aca      578
84 Met Asn Thr Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr
85              155              160              165
87 gtg cct ctc tct caa ggc ccc aaa cca gta atc agt ttt gcc aat      626
88 Val Pro Leu Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn
89              170              175              180
91 cac act tcc tgc cga tgc atg tct aaa ctg gat gtt tac aga caa gtt      674
92 His Thr Ser Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val
93              185              190              195
95 cat tcc att att aga cgt tcc ctg cca gca aca cta cca cag tgt cag      722
96 His Ser Ile Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln
97              200              205              210
99 gca gcg aac aag acc tgc ccc acc aat tac atg tgg aat aat cac atc      770
100 Ala Ala Asn Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile
101 215              220              225              230
103 tgc aga tgc ctg gct cag gaa gat ttt atg ttt tcc tcg gat gct gga      818
104 Cys Arg Cys Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly
105              235              240              245
107 gat gac tca aca gat gga ttc cat gac atc tgt gga cca aac aag gag      866
108 Asp Asp Ser Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu
109              250              255              260
111 ctg gat gaa gag acc tgt cag tgt gtc tgc aga gcg ggg ctt cgg cct      914
112 Leu Asp Glu Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro
113              265              270              275
115 gcc agc tgt gga ccc cac aaa gaa cta gac aga aac tca tgc cag tgt      962
116 Ala Ser Cys Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys
117              280              285              290
119 gtc tgt aaa aac aaa ctc ttc ccc agc caa tgt ggg gcc aac cga gaa      1010
120 Val Cys Lys Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu
121 295              300              305              310
123 ttt gat gaa aac aca tgc cag tgt gta tgt aaa aga acc tgc ccc aga      1058
124 Phe Asp Glu Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg
125              315              320              325
127 aat caa ccc cta aat cct gga aaa tgt gcc tgt gaa tgt aca gaa agt      1106

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128 Asn Gln Pro Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser
129          330          335          340
131 cca cag aaa tgc ttg tta aaa gga aag aag ttc cac cac caa aca tgc      1154
132 Pro Gln Lys Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys
133          345          350          355
135 agc tgt tac aga cgg cca tgt acg aac cgc cag aag gct tgt gag cca      1202
136 Ser Cys Tyr Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro
137          360          365          370
139 gga ttt tca tat agt gaa gaa gtg tgt cgt tgt gtc cct tca tat tgg      1250
140 Gly Phe Ser Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp
141          375          380          385          390
143 caa aga cca caa atg agc taagattgta ctgttttcca gttcatcgat      1298
144 Gln Arg Pro Gln Met Ser
145          395
147 tttctattat gaaaaactgt gttgccacag tagaactgtc tgtgaacaga gagacccttg      1358
149 tgggtccatg ctaacaaaga caaaagtctg tctttcctga accatgtgga taactttaca      1418
151 gaaatggact ggagctcatc tgcaaaaggc ctcttgtaaa gactgggtttt ctgccaatga      1478
153 ccaaacagcc aagattttcc tcttggtgatt tctttaaaag aatgactata taattttatt      1538
155 ccactaaaaa tattgtttct gcatttcatt ttatagcaac aacaattggt aaaactcact      1598
157 gtgatcaata tttttatc atgcaaaata tgtttaaaat aaaatgaaaa ttgtatttat      1658
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163 <211> LENGTH: 419
164 <212> TYPE: PRT
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167 <400> SEQUENCE: 2
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173 Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Phe
174          -5          -1 1          5
177 Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
178          10          15          20          25
181 Thr Ala Tyr Ala Ser Lys Asp Leu Glu Gln Leu Arg Ser Val Ser
182          30          35          40
185 Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
186          45          50          55
189 Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
190          60          65          70
193 Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
194          75          80          85
197 His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
198          90          95          100          105
201 Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
202          110          115          120
205 Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
206          125          130          135
209 Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
210          140          145          150
213 Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu

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214      155      160      165
217 Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
218 170      175      180      185
221 Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
222      190      195      200
225 Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
226      205      210      215
229 Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
230      220      225      230
233 Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
234      235      240      245
237 Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
238 250      255      260      265
241 Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
242      270      275      280
245 Gly Pro His Lys Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
246      285      290      295
249 Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
250      300      305      310
253 Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
254      315      320      325
257 Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
258 330      335      340      345
261 Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
262      350      355      360
265 Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
266      365      370      375
269 Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Gln Arg Pro
270      380      385      390
273 Gln Met Ser
274      395
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278 <211> LENGTH: 1525
279 <212> TYPE: DNA
280 <213> ORGANISM: Homo sapiens
282 <220> FEATURE:
283 <221> NAME/KEY: sig_peptide
284 <222> LOCATION: (71)..(142)
286 <220> FEATURE:
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288 <222> LOCATION: (71)..(1120)
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292 <222> LOCATION: (143)..()
294 <400> SEQUENCE: 3
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297 agatgaactc atg act gta ctc tac cca gaa tat tgg aaa atg tac aag 109
298 Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys
299 -20 -15

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| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 301 | tgt | cag | cta | agg | aaa | gga | ggc | tgg | caa | cat | aac | aga | gaa | cag | gcc | aac | 157 |
| 302 | Cys | Gln | Leu | Arg | Lys | Gly | Gly | Trp | Gln | His | Asn | Arg | Glu | Gln | Ala | Asn | |
| 303 | | -10 | | | | | -5 | | | | -1 | 1 | | | | 5 | |
| 305 | ctc | aac | tca | agg | aca | gaa | gag | act | ata | aaa | ttt | gct | gca | gca | cat | tat | 205 |
| 306 | Leu | Asn | Ser | Arg | Thr | Glu | Glu | Thr | Ile | Lys | Phe | Ala | Ala | Ala | His | Tyr | |
| 307 | | | | | 10 | | | | | 15 | | | | | 20 | | |
| 309 | aat | aca | gag | atc | ttg | aaa | agt | att | gat | aat | gag | tgg | aga | aag | act | caa | 253 |
| 310 | Asn | Thr | Glu | Ile | Leu | Lys | Ser | Ile | Asp | Asn | Glu | Trp | Arg | Lys | Thr | Gln | |
| 311 | | | | | 25 | | | | 30 | | | | | 35 | | | |
| 313 | tgc | atg | cca | cgg | gag | gtg | tgt | ata | gat | gtg | ggg | aag | gag | ttt | gga | gtc | 301 |
| 314 | Cys | Met | Pro | Arg | Glu | Val | Cys | Ile | Asp | Val | Gly | Lys | Glu | Phe | Gly | Val | |
| 315 | | | | | 40 | | | | 45 | | | | 50 | | | | |
| 317 | gcg | aca | aac | acc | ttc | ttt | aaa | cct | cca | tgt | gtg | tcc | gtc | tac | aga | tgt | 349 |
| 318 | Ala | Thr | Asn | Thr | Phe | Phe | Lys | Pro | Pro | Cys | Val | Ser | Val | Tyr | Arg | Cys | |
| 319 | | 55 | | | | | 60 | | | | | 65 | | | | | |
| 321 | ggg | ggt | tgc | tgc | aat | agt | gag | ggg | ctg | cag | tgc | atg | aac | acc | agc | acg | 397 |
| 322 | Gly | Gly | Cys | Cys | Asn | Ser | Glu | Gly | Leu | Gln | Cys | Met | Asn | Thr | Ser | Thr | |
| 323 | 70 | | | | | | 75 | | | | 80 | | | | 85 | | |
| 325 | agc | tac | ctc | agc | aag | acg | tta | ttt | gaa | att | aca | gtg | cct | ctc | tct | caa | 445 |
| 326 | Ser | Tyr | Leu | Ser | Lys | Thr | Leu | Phe | Glu | Ile | Thr | Val | Pro | Leu | Ser | Gln | |
| 327 | | | | | 90 | | | | | 95 | | | | 100 | | | |
| 329 | ggc | ccc | aaa | cca | gta | aca | atc | agt | ttt | gcc | aat | cac | act | tcc | tgc | cga | 493 |
| 330 | Gly | Pro | Lys | Pro | Val | Thr | Ile | Ser | Phe | Ala | Asn | His | Thr | Ser | Cys | Arg | |
| 331 | | | | | 105 | | | | 110 | | | | 115 | | | | |
| 333 | tgc | atg | tct | aaa | ctg | gat | gtt | tac | aga | caa | gtt | cat | tcc | att | att | aga | 541 |
| 334 | Cys | Met | Ser | Lys | Leu | Asp | Val | Tyr | Arg | Gln | Val | His | Ser | Ile | Ile | Arg | |
| 335 | | 120 | | | | | 125 | | | | | 130 | | | | | |
| 337 | cgt | tcc | ctg | cca | gca | aca | cta | cca | cag | tgt | cag | gca | gcg | aac | aag | acc | 589 |
| 338 | Arg | Ser | Leu | Pro | Ala | Thr | Leu | Pro | Gln | Cys | Gln | Ala | Ala | Asn | Lys | Thr | |
| 339 | | 135 | | | | | 140 | | | | 145 | | | | | | |
| 341 | tgc | ccc | acc | aat | tac | atg | tgg | aat | aat | cac | atc | tgc | aga | tgc | ctg | gct | 637 |
| 342 | Cys | Pro | Thr | Asn | Tyr | Met | Trp | Asn | Asn | His | Ile | Cys | Arg | Cys | Leu | Ala | |
| 343 | 150 | | | | | 155 | | | | | 160 | | | | 165 | | |
| 345 | cag | gaa | gat | ttt | atg | ttt | tcc | tgc | gat | gct | gga | gat | gac | tca | aca | gat | 685 |
| 346 | Gln | Glu | Asp | Phe | Met | Phe | Ser | Ser | Asp | Ala | Gly | Asp | Asp | Ser | Thr | Asp | |
| 347 | | | | | 170 | | | | | 175 | | | | 180 | | | |
| 349 | gga | ttc | cat | gac | atc | tgt | gga | cca | aac | aag | gag | ctg | gat | gaa | gag | acc | 733 |
| 350 | Gly | Phe | His | Asp | Ile | Cys | Gly | Pro | Asn | Lys | Glu | Leu | Asp | Glu | Glu | Thr | |
| 351 | | | | | 185 | | | | 190 | | | | 195 | | | | |
| 353 | tgt | cag | tgt | gtc | tgc | aga | gcg | ggg | ctt | cgg | cct | gcc | agc | tgt | gga | ccc | 781 |
| 354 | Cys | Gln | Cys | Val | Cys | Arg | Ala | Gly | Leu | Arg | Pro | Ala | Ser | Cys | Gly | Pro | |
| 355 | | | | | 200 | | | | 205 | | | | 210 | | | | |
| 357 | cac | aaa | gaa | cta | gac | aga | aac | tca | tgc | cag | tgt | gtc | tgt | aaa | aac | aaa | 829 |
| 358 | His | Lys | Glu | Leu | Asp | Arg | Asn | Ser | Cys | Gln | Cys | Val | Cys | Lys | Asn | Lys | |
| 359 | | 215 | | | | | 220 | | | | | 225 | | | | | |
| 361 | ctc | ttc | ccc | agc | caa | tgt | ggg | gcc | aac | cga | gaa | ttt | gat | gaa | aac | aca | 877 |
| 362 | Leu | Phe | Pro | Ser | Gln | Cys | Gly | Ala | Asn | Arg | Glu | Phe | Asp | Glu | Asn | Thr | |
| 363 | 230 | | | | | 235 | | | | | 240 | | | | 245 | | |
| 365 | tgc | cag | tgt | gta | tgt | aaa | aga | acc | tgc | ccc | aga | aat | caa | ccc | cta | aat | 925 |

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.



VERIFICATION SUMMARY

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DATE: 02/07/2002

TIME: 13:34:46

Input Set : A:\PF112P3D1C1subSL.txt

Output Set: N:\CRF3\02072002\I935726.raw

L:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8